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# UniProtKB/TrEMBL entry Q0PBL7

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[Entry history](#)

[Entry info] [Name and origin] [References] [Comments] [Cross-references]  
[Keywords] [Features] [Sequence] [Tools]

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## Entry information

Entry name	Q0PBL7_CAMJE
Primary accession number	Q0PBL7
Secondary accession numbers	None
Integrated into TrEMBL on	September 19, 2006
Sequence was last modified on	September 19, 2006 (Sequence version 1)
Annotations were last modified on	July 22, 2008 (Entry version 13)
Name and origin of the protein	
Protein name	Major antigenic peptide PEB3 [Precursor]
Synonyms	None
Gene name	Name: <i>peb3</i> OrderedLocusNames: <i>Cj0289c</i>
From	<i>Campylobacter jejuni</i> [TaxID: 197] [HAMAP proteome]
Taxonomy	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales; Campylobacteraceae; Campylobact
Protein existence	1: Evidence at protein level;

## References

- [1] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 STRAIN=NCTC 11168 / Serotype O:2;  
 DOI=10.1038/35001088; PubMed=10688204 [NCBI, ExPASy, EBI, Israel, Japan]  
 Parkhill J., Wren B.W., Mungall K.L., Ketley J.M., Churcher C.M., Basham D., Chillingworth  
 Davies R.M., Feltwell T., Holroyd S., Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Per  
 C.W., Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M., Whitehead S., Be

B.G.;

"The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hypervariable sequences.";

Nature 403:665-668(2000).

#### Comments

- INTERACTION:**

Q0PBH3:motB; NbExp=1; IntAct=EBI-1192366, EBI-1191146;

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#### Cross-references

##### Sequence databases

EMBL	AL111168; CAL34442.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]
PIR	G81447; G81447.	

##### 3D structure databases

PDB	2HXW; X-ray; 1.60 A; A/B=21-250.[ExpASY / RCSB / EBI]
PDBsum	2HXW; -.
ModBase	Q0PBL7.

##### Protein-protein interaction databases

IntAct Q0PBL7; -.

##### Ontologies

GO:0005515; Molecular function: protein binding (*inferred from physical interaction from IntAct*).

##### GO

QuickGo  
view.

##### Genome annotation databases

GenomeReviews AL111168\_GR; Cj0289c.

KEGG cje:Cj0289c; -.

##### Phylogenomic databases

HOGENOM Q0PBL7; -.

##### Genome annotation databases

CMR Q0PBL7; Cj0289c.

##### Other

UniRef View cluster of proteins with at least 50% / 90% / 100% identity.

#### Keywords

Complete proteome; Signal.

#### Features



Feature table viewer

Key	From	To	Length	Description	FTId
SIGNAL	1	20	20	Potential.	

CHAIN 21 250 230 Potential. PRO\_5000074997

## Sequence information

Length: 250 AA [This is the length of the unprocessed precursor] Molecular weight: 27537 Da [This is the MW of the unprocessed precursor] CRC64: B2A9AF0630A04065 is a checksum on the sequence

10	20	30	40	50	60
MKKIITLFGA	CALAFSMA	DNVLYGPGGP	HTALKDIANK	YSEKTGVKVN	VNFGPQATWF
70	80	90	100	110	120
EKAKKADAIL	FGASDQSALA	IASDFGKDFN	VSKIKPLYFR	EAIILTQKGN	PLKIKGLKDL
130	140	150	160	170	180
ANKKVRIVVP	EGAGKSNITSG	TGVWEDMIGR	TQDIKTIQNF	RNNIVAFVFN	SGSARKLFAQ
190	200	210	220	230	240
DQADAWITWI	DWSKSNPDIG	TAVAIEKDLV	VYRTFNVIK	EGASKETQDF	IAYLSSKEAK
250					
EIFKKYGWRE					

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in  
F/  
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BLAST

BLAST submission on  
ExPASy/SIB  
or at NCBI (USA)



Sequence analysis tools: ProtParam,  
ProtScale, Compute pI/Mw, PeptideMass,  
PeptideCutter, Dotlet (Java)



ScanProsite, MotifScan



Submit a homology modeling request to  
SWISS-MODEL



NPSC Sequence  
analysis tools

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